

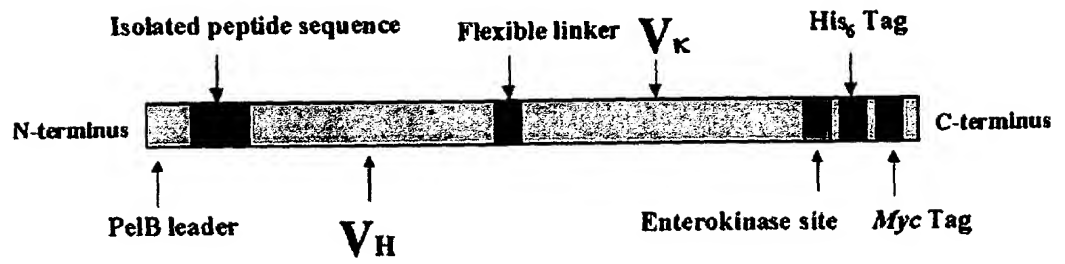
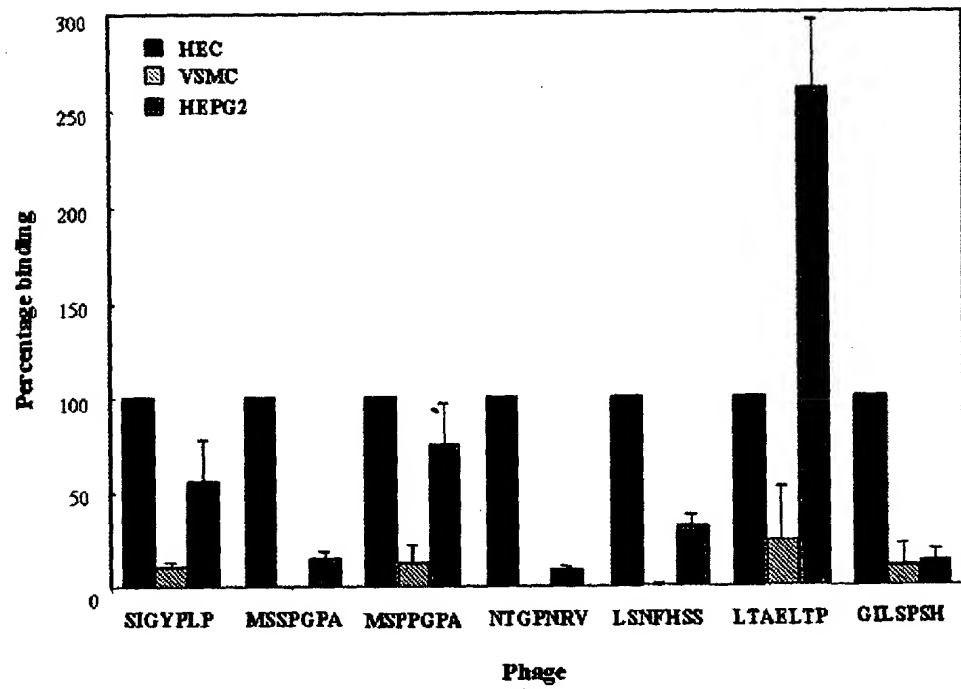
FIGURE 1**FIGURE 2**

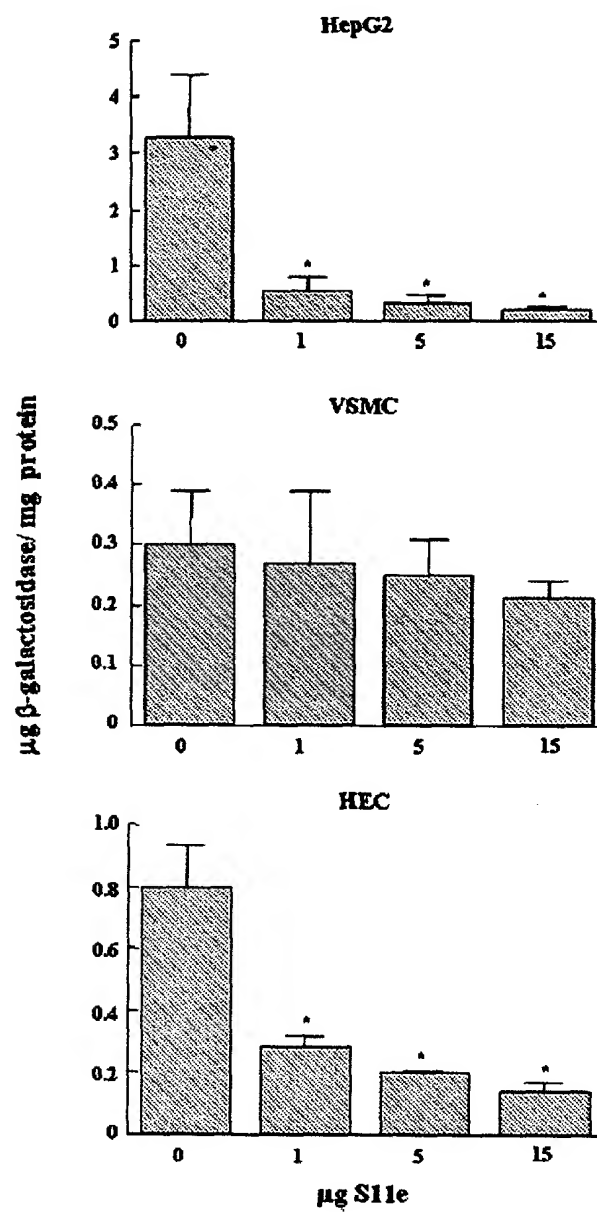
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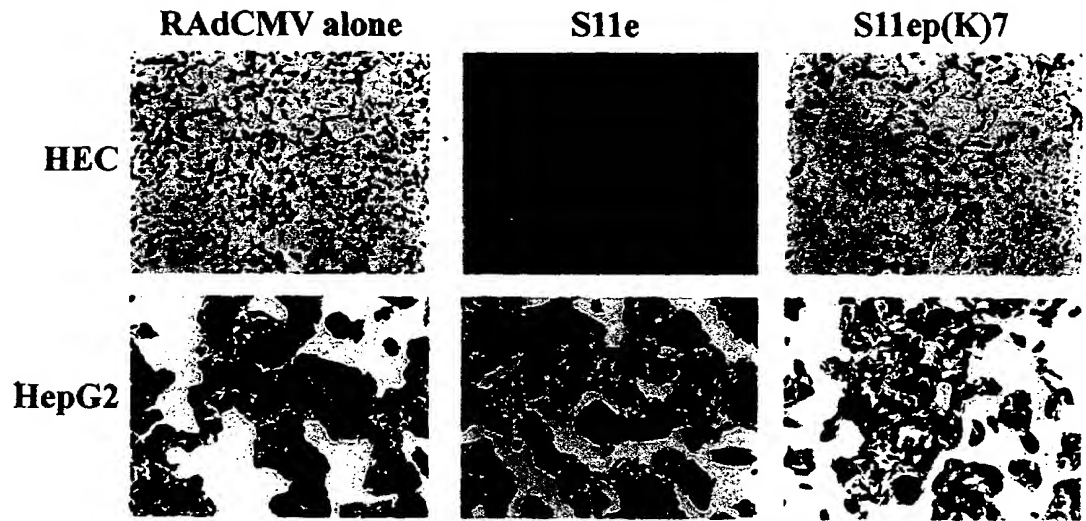
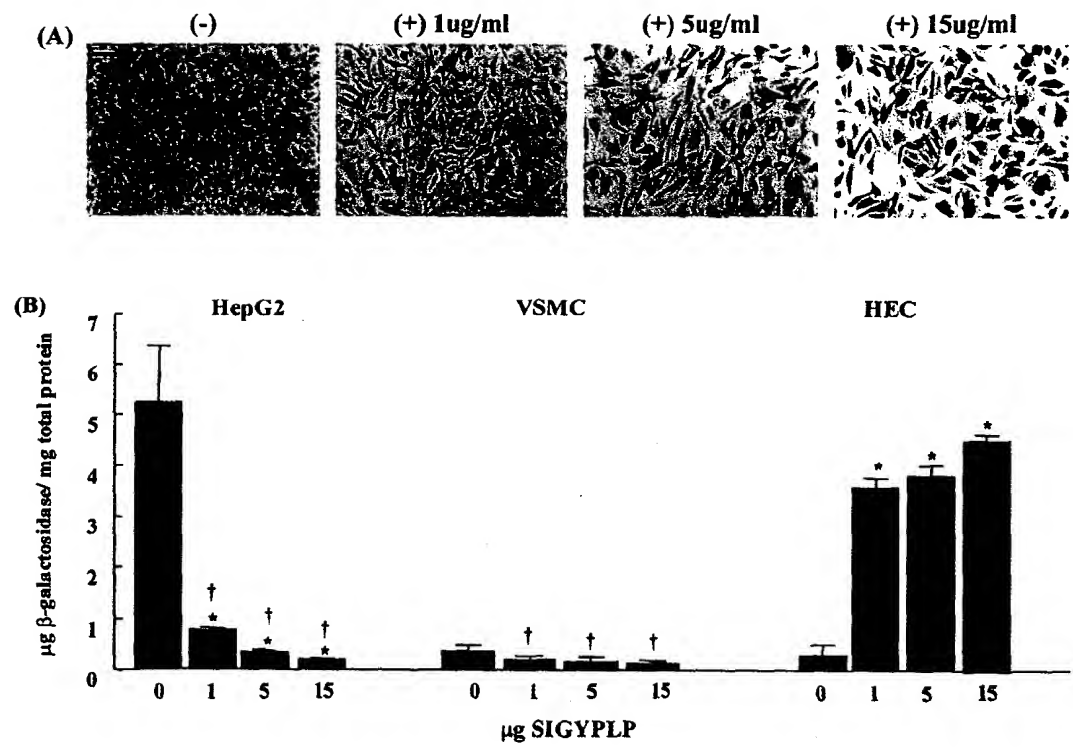
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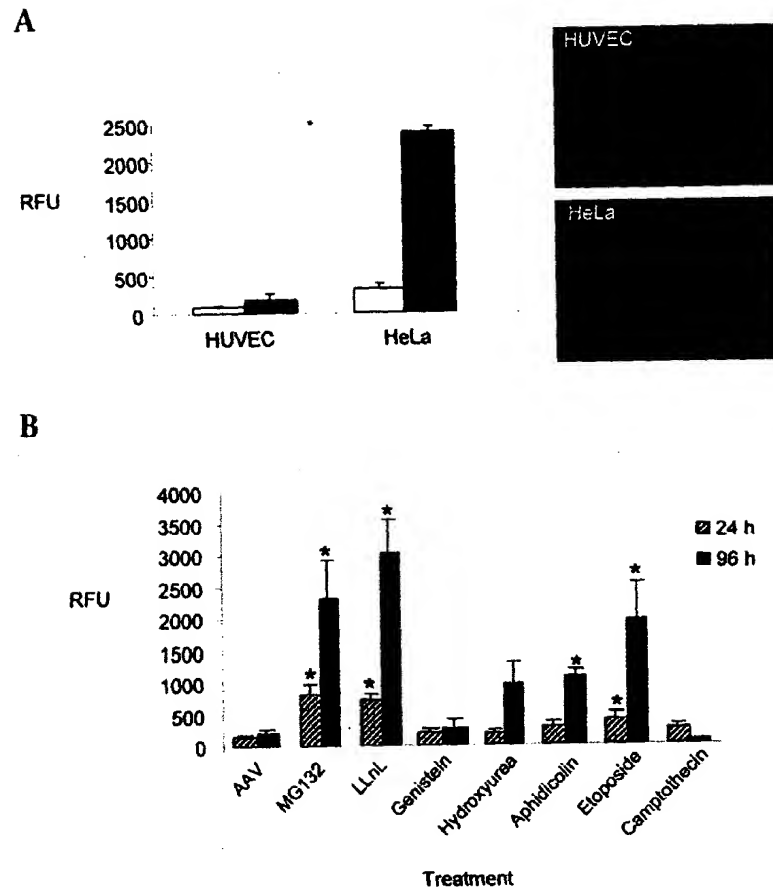
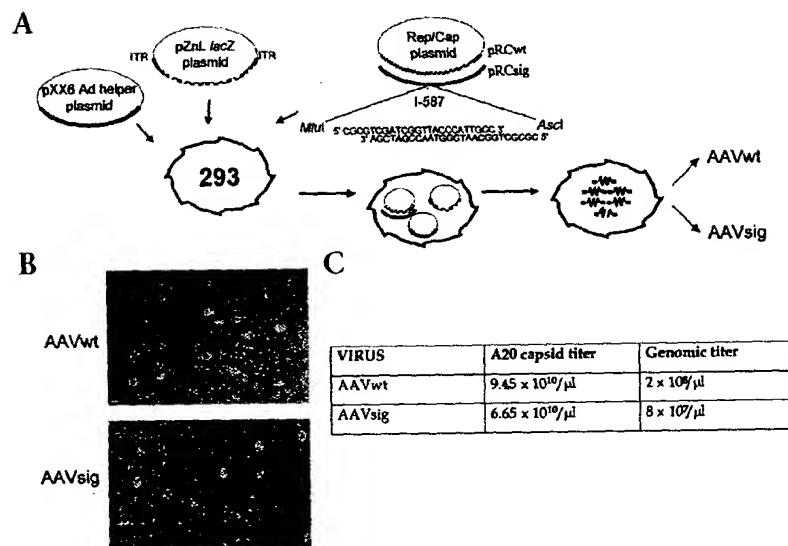
FIGURE 6**FIGURE 7**

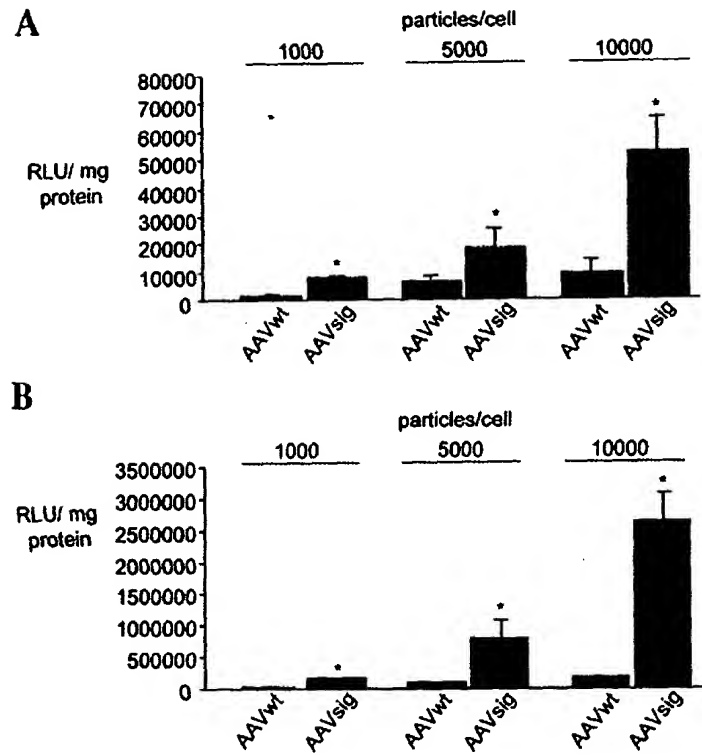
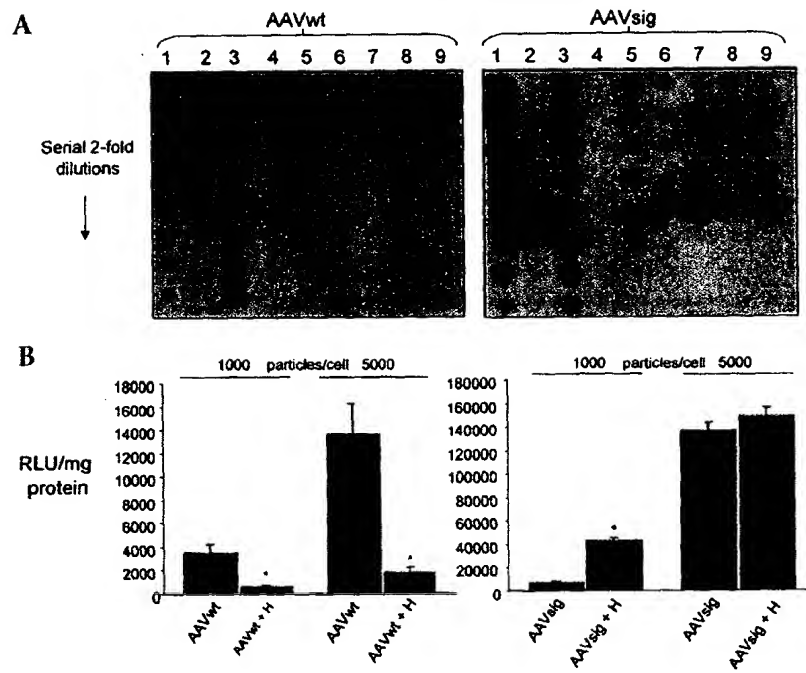
FIGURE 8**FIGURE 9**

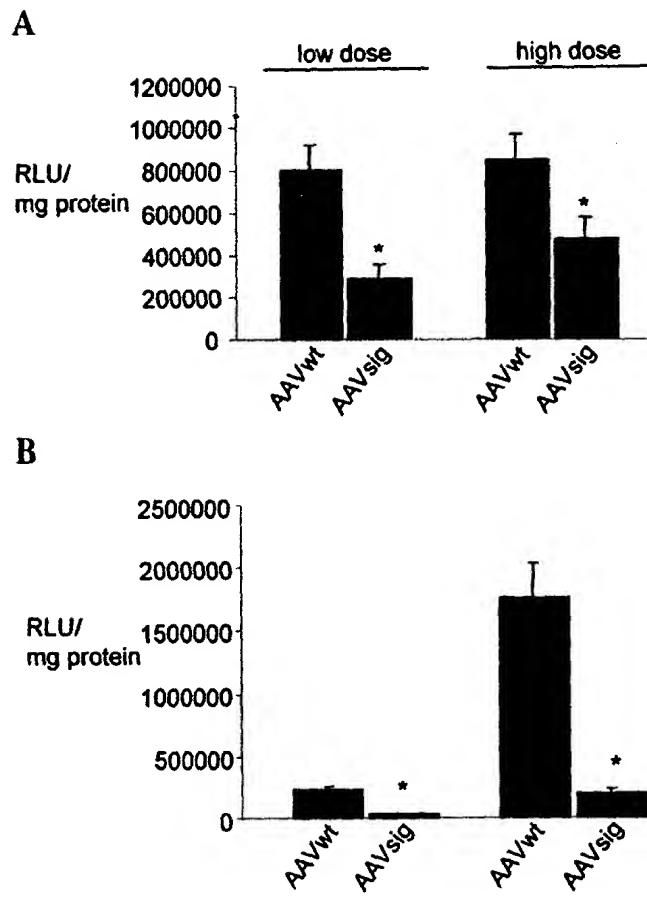
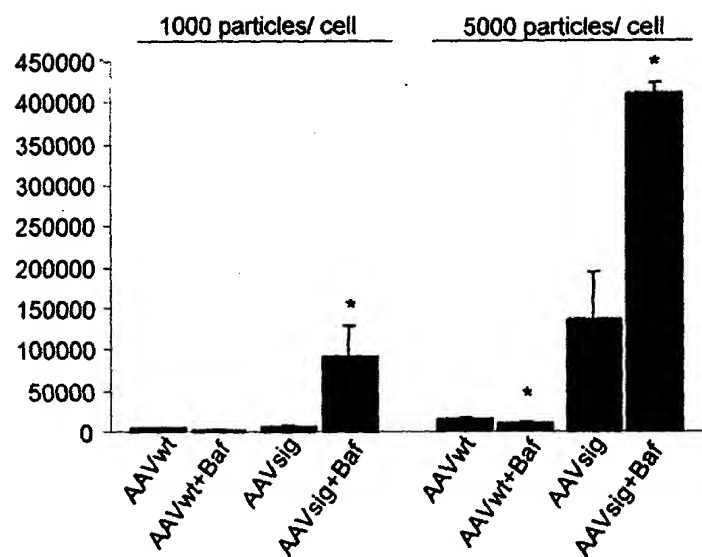
FIGURE 10**FIGURE 11**

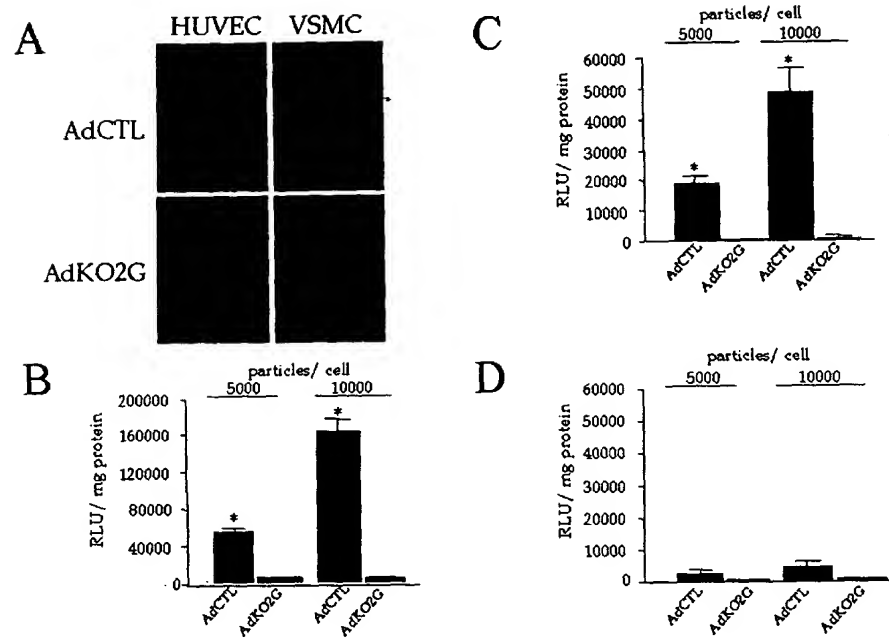
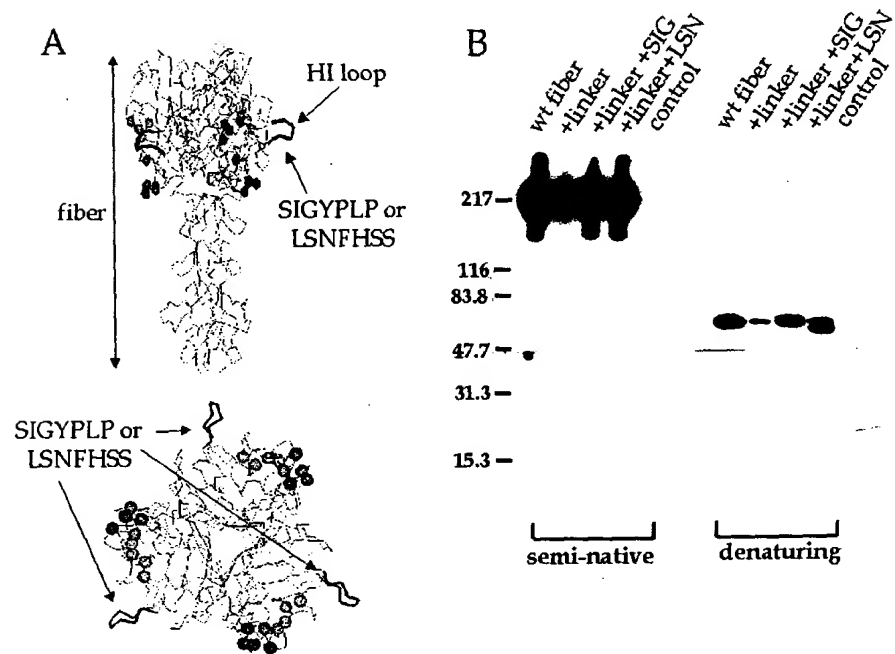
FIGURE 12**FIGURE 13**

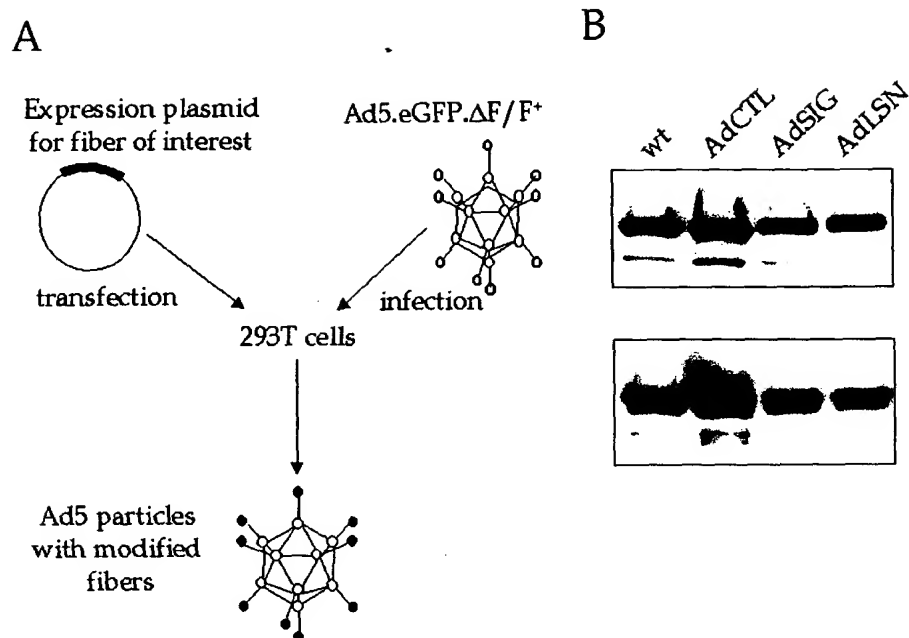
FIGURE 14

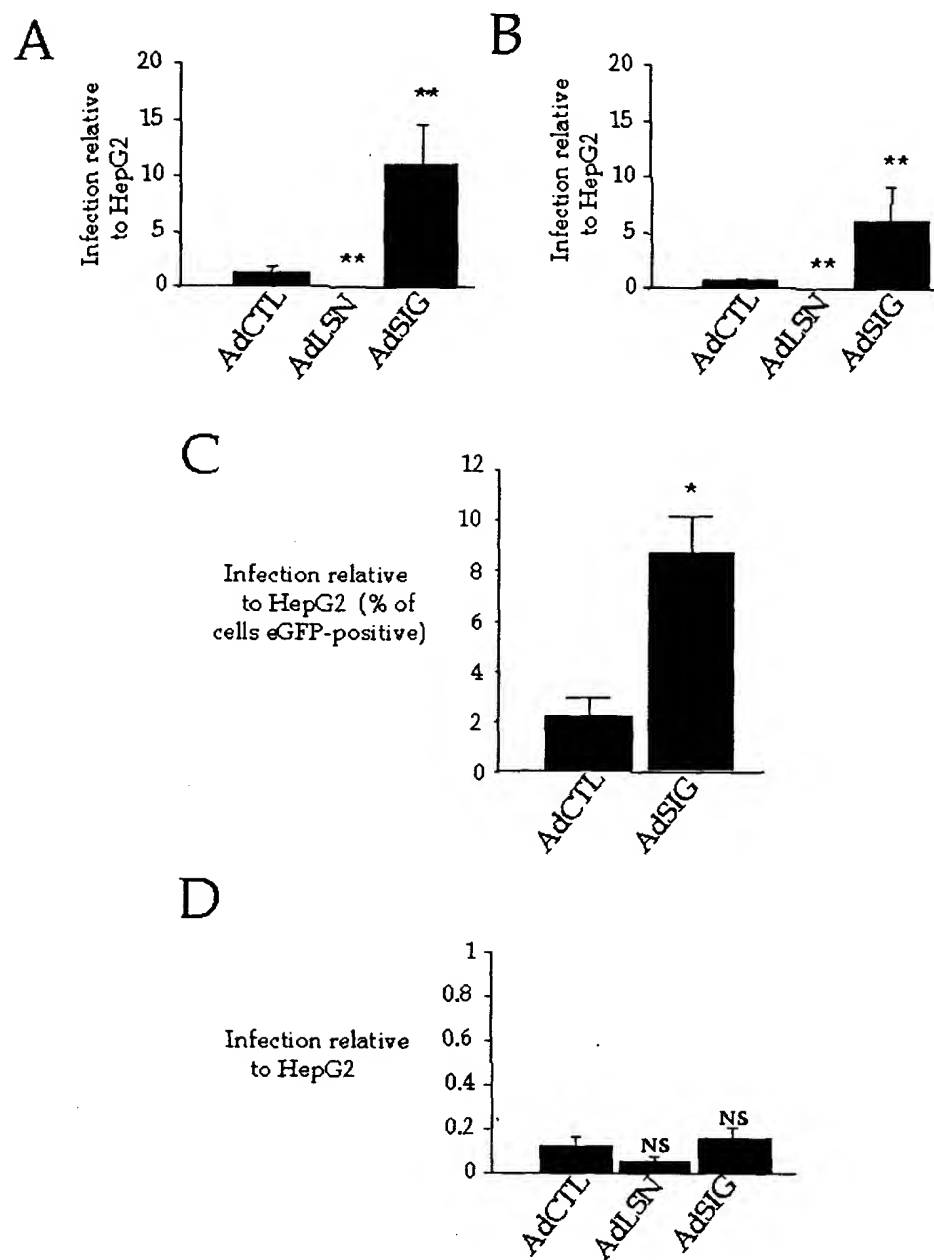
FIGURE 15

FIGURE 16

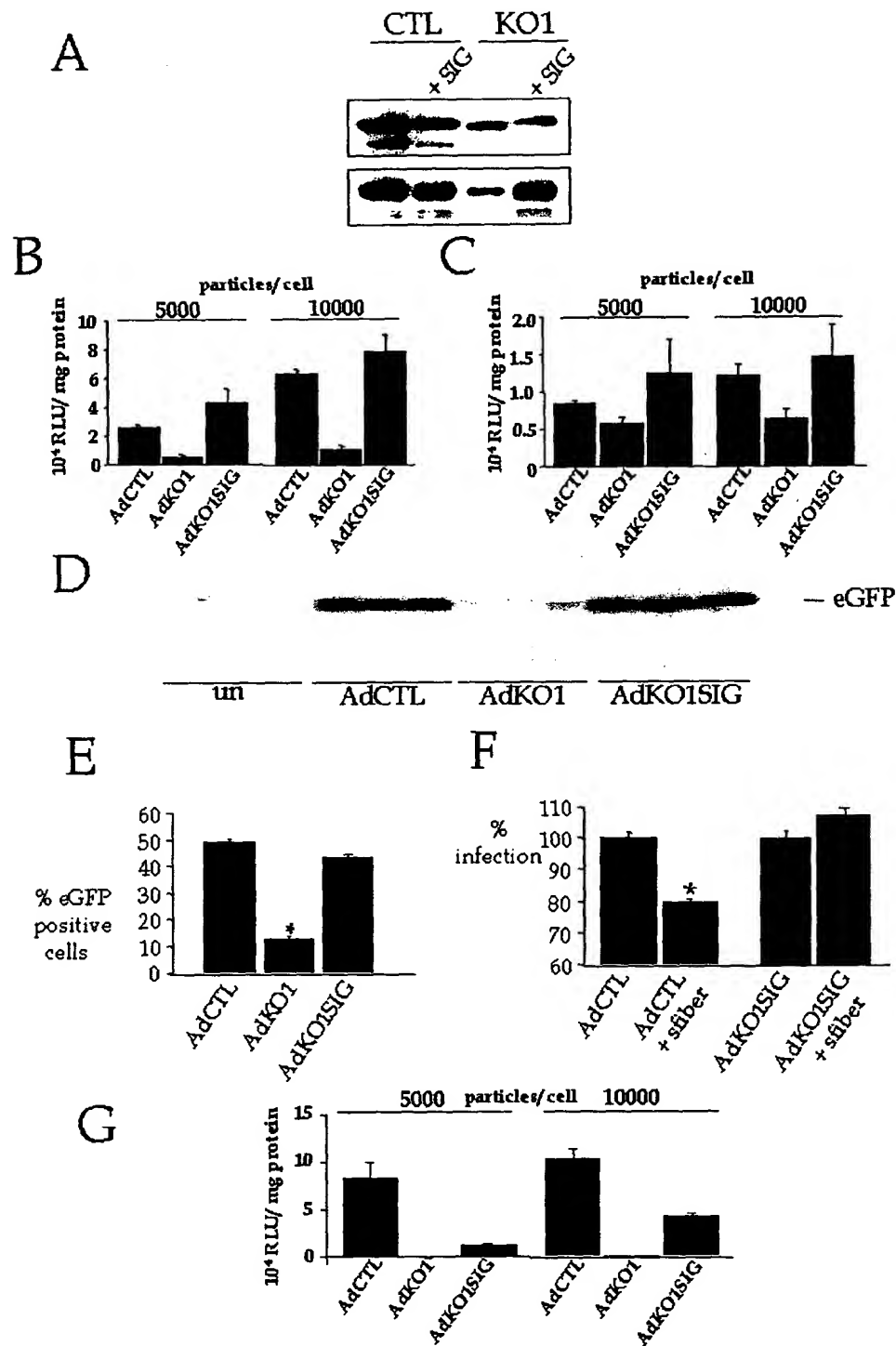


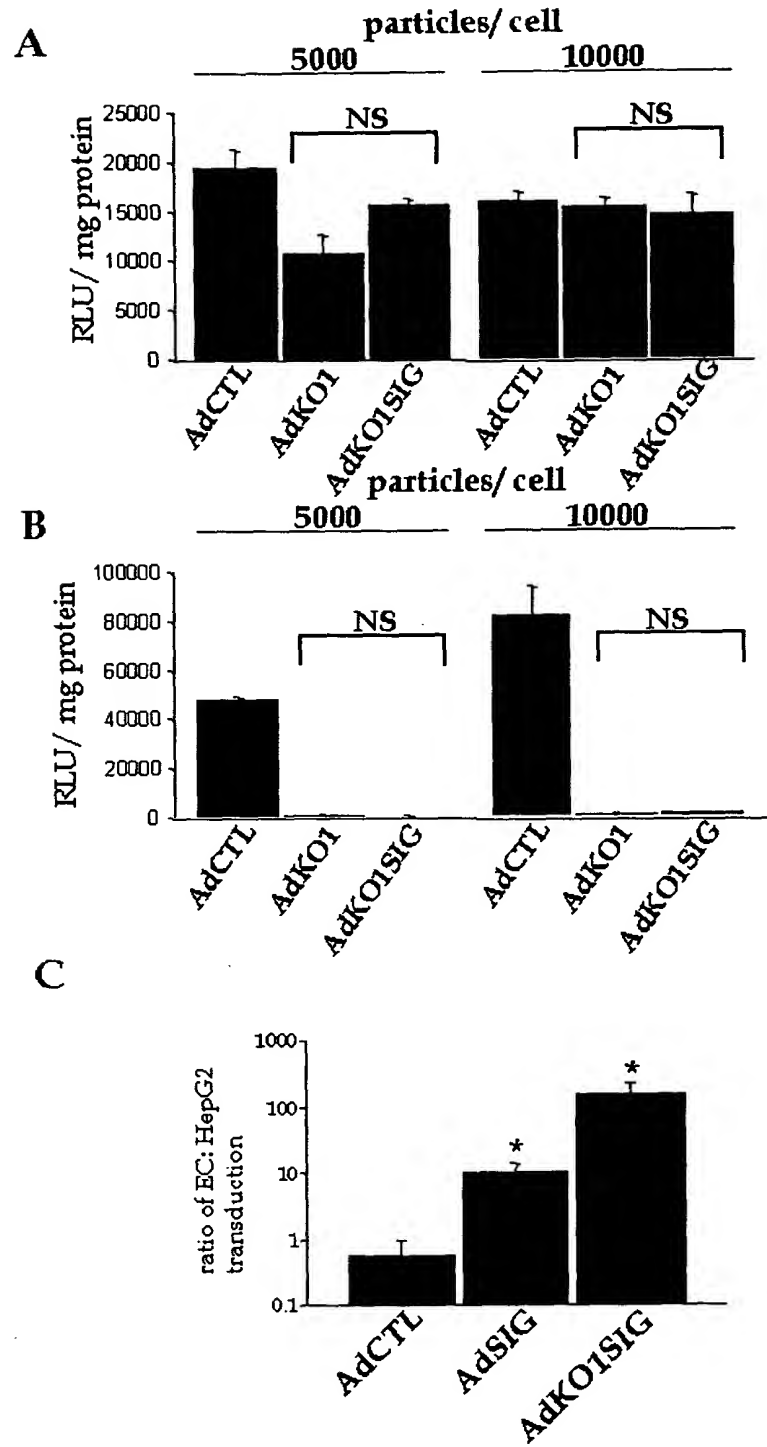
FIGURE 17

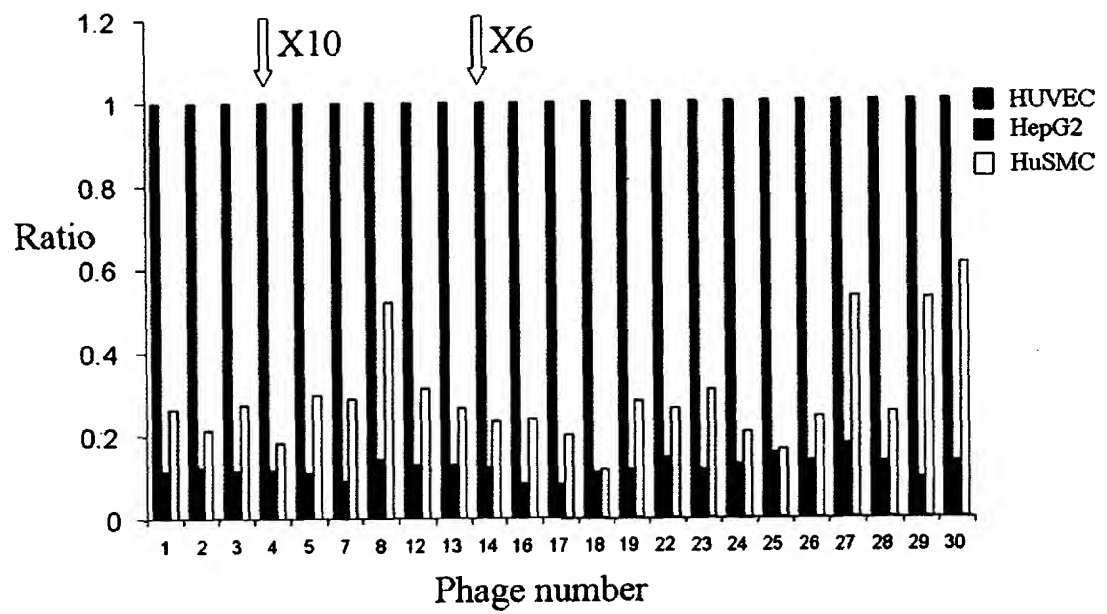
FIGURE 18

FIGURE 19

1	5	----	MSNNPIRPPTS	G-	12	39	25	----	LSTPLPYDMRR	S-	12
2	10	----	MSNNPIRPPTS	G-	12	40	4	--	MSLTTPPAVARP-	--	12
3	27	----	MSTPPIREQAA	H-	12						
4	22	----	MSQTPYARPQY	V-	12	41	6	--	MSLTTPPAVARP-	--	12
						42	9	--	MSLTTPPAVARP-	--	12
5	53	---	MSSPTVSSAPQY	--	12	43	11	--	MSLTTPPAVARP-	--	12
6	39	---	LQPPSMITHPST	--	12	44	15	--	MSLTTPPAVARP-	--	12
7	43	---	LQPPSMITHPST	--	12						
8	1	--	MAMPQPADHNNS-	--	12	45	33	--	MSLTTPPAVARP-	--	12
						46	34	--	MSLTTPPAVARP-	--	12
9	45	--	MLMPQPAHHNNS-	--	12	47	41	--	MSLTTPPAVARP-	--	12
10	67	--	MGMTVPENLIVQ-	--	12	48	47	--	MSLTTPPAVARP-	--	12
11	68	--	MGMTVPENLIVQ-	--	12						
12	2	-V	SGMSVPVQLAR--	--	12	49	48	--	MSLTTPPAVARP-	--	12
						50	42	----	LTPPNQVLNPL	Y-	12
13	3	---	MTQTPR-TTPWP	D-	12	51	29	---	MTPIATSI PPQM	--	12
14	28	---	MTNLPT-VTQFP	P-	12	52	35	---	MTQQPPLPHPAK	--	12
15	23	---	MTSNPH-LNPGP	R-	12						
16	52	--	SMRGLPE-LNPRI	--	12	53	58	---	MAINDTYPPPRP	--	12
						54	32	----	MTSPHPQTPNL	T-	12
17	63	LT	SPFSTP--LNPR-	--	12	55	54	---	VLSMQTPPTPLL	--	12
18	70	LT	SPFSTP--LNPR-	--	12	56	30	--	MTPTTPIPSLPQ-	--	12
19	8	---	MTGSQQTLHPPP	--	12						
20	61	---	MQPRPQTLTPAS	--	12	57	24	--	MGHNINIPRTPL-	--	12
						58	60	---	LAQNPIYRAHPH	--	12
21	26	---	MTRIQDSPYDLR	--	12	59	62	----	LTVPVVVSFAV	H-	12
22	69	---	MTPIQSTQYPHS	--	12	60	66	----	ANTPPHTILST	E-	12
23	13	---	MNMTPPPHSPPK	--	12						
24	16	--	AMSMTTMPHSPN-	--	12	61	17	---	MSDLLIEYPPYI	--	12
						62	18	----	MTLPHEL RDGA	L-	12
25	14	----	MTPFPTSNEA	NL	12	63	36	----	LAKPLPTTSNT	G-	12
26	20	----	MTPFPTSNEA	NL	12	64	37	----	LSKPIPHIPSS	IG	13
27	31	----	MTPFPTSNEA	NL	12						
28	40	----	MTPFPTSNEA	NL	12	65	49	---	SSRIPGFDPDLH	--	12
						66	38	---	CICRGVGCCLLL	--	12
29	51	----	MTPFPTSNEA	NL	12	67	44	----	AFPMVG GPDH	FR	12
30	57	----	MTPFPTSNEA	NL	12	68	46	---	AQAMANPLGSHI	--	12
31	21	-----	NPEPTIDE-	--	8						
32	64	-----	NPEPTIDE-	--	8	69	55	----	THAMSHLDKAH	--	11
						70	50	-----		--	0
33	7	-MT	QVYTPPPTST--	--	12						
34	59	----	MMPPPTSLPS	PS	12						
35	12	---	MATQPLSGSRLS	G-	13						
36	65	---	MAGQPKDSSKTL	--	12						
37	56	---	MAVQPPNTSTSN	--	12						
38	19	----	AAVPPPYVMSR	P-	12						

1234567891011121314151617181920212223242526272829303132333435363738
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FIGURE 20

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---MAGQPKDSSKTL---
---MQPRPQTLTPAS---
---MTNLPT-VTQFPF---
---MSSPTVSSAPQY---
---LTPPNQVLNPLY---
---MTPIATSIPPQM---
---MTSPHPQTPNLT---
---VLSMQTPPTPLL---
---MGHNINIPRTPL---
---LAQNPIYRAHPH---
---LTPVPVVSFAVH---
---ANTPPHTILSTE---
---MSDLLIEYPPYI---
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